

68  
SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANTS: Iris Pecker et al.
- (ii) TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES AND THEIR USE IN RESEARCH AND MEDICAL APPLICATIONS
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: G. E. Ehrlich (1995) Ltd.  
c/o Anthony Castorina  
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Arlington  
Virginia  
United States of America  
22202
- (B) STREET:
- (C) CITY:
- (D) STATE:
- (E) COUNTRY:
- (F) ZIP:
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
- (B) COMPUTER: Twinhead\* Slimnote-890TX
- (C) OPERATING SYSTEM: MS DOS version 6.2,  
Windows version 3.11
- (D) SOFTWARE: Word for Windows version 2.0 converted to an ASCII file
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/922,180
- (B) FILING DATE: September 2, 1997
- (A) APPLICATION NUMBER: 09/071,739
- (B) FILING DATE: May 1, 1998
- (A) APPLICATION NUMBER: 09/322,977
- (B) FILING DATE: June 1, 1999
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Sol Sheinbein
- (B) REGISTRATION NUMBER: 25,457
- (C) REFERENCE/DOCKET NUMBER: 00/21505
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 972-3-6127676
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- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1721
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CTAGAGCTTT CGACTCTCCG CTGCGCGGCA GCTGGCGGGG GGAGCAGCCA GGTGAGCCCA 60
AGATGCTGCT GCGCTCGAAG CCTGCGCTGC CGCCGCGGCT GATGCTGCTG CTCCTGGGGC 120
CGCTGGGTCC CCTCTCCCTT GCGGCCCTGC CCCGACCTGC GCAAGCACAG GACGTCGTGG 180
ACCTGGGACTT cTTcACCCAG GAGCCGCTGC ACCTGGGTGAG CCCCTCGTTC CTGTCCGTCA 240
CCATTGACGC CAACCTGGCC ACGGACCCGC GGTTCCTCAT CCTCCTGGGT TCTCCAAAGC 300
TTCGTACCTT GGCCAGAGGC TTGCTCTCTG CGTACCTGAG GTTTGGTGGC ACCAAGACAG 360
ACTTCCTAAT TTTCGATCCC AAGAAGGAAT CAACCTTTGA AGAGAGAAGT TACTGGCAAT 420
CTCAAGTCAA CCAGGATATT TGCAAATATG GATCCATCCC TCCTGATGTG GAGGAGAAGT 480
TACGGTTGGA ATGGCCCTAC CAGGAGCAAT TGCTACTCCG AGAACACTAC CAGAAAAAGT 540
TCAAGAACAG CACCTACTCA AGAAGCTCTG TAGATGTGCT ATACACTTTT GCAAACTGCT 600
CAGGACTGGA CTTGATCTTT GGCCTAAATG CGTTATTAAG AACAGCAGAT TTGCAGTGGA 660
ACAGTTCTAA TGCTCAGTTG CTCCTGGACT ACTGCTCTTC CAAGGGGTAT AACATTTCTT 720
GGGAACCTAGG CAATGAACCT AACAGTTTCC TTAAGAAGGC TGATATTTTC ATCAATGGGT 780
CGCAGTTAGG AGAAGATTAT ATTCAATTGC ATAACTTCTT AAGAAAGTCC ACCTTCAAAA 840
ATGCAAAACT CTATGGTCTT GATGTTGGTC AGCCTCGAAG AAAGACGGCT AAGATGCTGA 900
AGAGCTTCCT GAAGGCTGGT GGAGAAGTGA TTGATTGAGT TACATGGCAT CACTACTATT 960
TGAATGGACG GACTGCTACC AGGGAAGATT TTCTAAACCC TGATGTATTG GACATTTTAA 1020
TTTCACTCTG GCAAAAAGTT TTCCAGGTGG TTGAGAGCAC CAGGCCTGGC AAGAAGGTCT 1080
GGTTAGGAGA AACAAAGCTCT GCATATGGAG GCGGAGCGCC CTTGCTATCC GACACCTTTG 1140
CAGCTGGCTT TATGTGGCTG GATAAATTGG GCCTGTCAGC CCGAATGGGA ATAGAAGTGG 1200
TGATGAGGCA AGTATTCTTT TTCCAGGTGG TTGAGAGCAC CAGGCCTGGC AAGAAGGTCT 1260
CTTTACCTGA TTATTGGCTA TCTCTTCTGT TCAAGAAATT GGTGGGCACC AAGGTGTTAA 1320
TGCAAGCGTT GCAAGGTGTA AAGAGAAGGA AGCTTCGAGT ATACCTTCAT TGACACAAAC 1380
CTGACAAATC AAGGTATATA GAAGGAGATT TAACTCTGTA TGCCATAAAC CTCATAAGC 1440
TCACCAAGTA CTTGCGGTTA CCCTATCCTT TTTCTAACAA GCAAGTGGAT AAATACCTTC 1500
TAAGACCTTT GGGACCTCAT GGATTACTTT CCAAATCTGT CCAACTCAAT GGTCTAATC 1560
TAAAGATGGT GGATGATCAA ACCTTGCCAC CTTAATGGA AAAACCTCTC CGGCCAGGAA 1620
GTTCACTGGG CTTGCCAGCT TTCTCATATA GTTTTTTTGT GATAAGAAAT GCCAAAGTTG 1680
CTGCTTGCAT CTGAAATAAA AATATACTAG TCCTGACACT G 1721
```

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
      5                      10                      15

Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
      20                      25                      30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
      35                      40                      45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
      50                      55                      60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
      65                      70                      75                      80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
      85                      90                      95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
      100                     105                     110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
      115                     120                     125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
      130                     135                     140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
      145                     150                     155                     160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
      165                     170                     175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
      180                     185                     190

Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
      195                     200                     205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
      210                     215                     220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
      225                     230                     235                     240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
      245                     250                     255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
      260                     265                     270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
      275                     280                     285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
      290                     295                     300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
      305                     310                     315                     320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
      325                     330                     335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
      340                     345                     350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
      355                     360                     365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
      370                     375                     380

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00440-2034460

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro  
 385 390 395 400  
 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr  
 405 410 415  
 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg  
 420 425 430  
 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly  
 435 440 445  
 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu  
 450 455 460  
 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu  
 465 470 475 480  
 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn  
 485 490 495  
 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met  
 500 505 510  
 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser  
 515 520 525  
 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile  
 530 535 540 543

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1721  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CT AGA GCT TTC GAC 14  
 TCT CCG CTG CGC GGC AGC TGG CGG GGG GAG CAG CCA GGT GAG CCC AAG 62  
 ATG CTG CTG CGC TCG AAG CCT GCG CTG CCG CCG CCG CTG ATG CTG CTG 110  
 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu  
 5 10 15  
 CTC CTG GGG CCG CTG GGT CCC CTC TCC CCT GGC GCC CTG CCC CGA CCT 158  
 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro  
 20 25 30  
 GCG CAA GCA CAG GAC GTC GTG GAC CTG GAC TTC TTC ACC CAG GAG CCG 206  
 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro  
 35 40 45  
 CTG CAC CTG GTG AGC CCC TCG TTC CTG TCC GTC ACC ATT GAC GCC AAC 254  
 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
 50 55 60  
 CTG GCC ACG GAC CCG CGG TTC CTC ATC CTC CTG GGT TCT CCA AAG CTT 302  
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
 65 70 75 80  
 CGT ACC TTG GCC AGA GGC TTG TCT CCT GCG TAC CTG AGG TTT GGT GGC 350  
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
 85 90 95  
 ACC AAG ACA GAC TTC CTA ATT TTC GAT CCC AAG AAG GAA TCA ACC TTT 398  
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe  
 100 105 110  
 GAA GAG AGA AGT TAC TGG CAA TCT CAA GTC AAC CAG GAT ATT TGC AAA 446  
 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys  
 115 120 125  
 TAT GGA TCC ATC CCT CCT GAT GTG GAG GAG AAG TTA CGG TTG GAA TGG 494  
 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp  
 130 135 140  
 CCC TAC CAG GAG CAA TTG CTA CTC CGA GAA CAC TAC CAG AAA AAG TTC 542

Pro	Tyr	Gln	Glu	Gln	Leu	Leu	Leu	Arg	Glu	His	Tyr	Gln	Lys	Lys	Phe	
145					150					155					160	
AAG	AAC	AGC	ACC	TAC	TCA	AGA	AGC	TCT	GTA	GAT	GTG	CTA	TAC	ACT	TTT	590
Lys	Asn	Ser	Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe	
				165					170					175		
GCA	AAC	TGC	TCA	GGA	CTG	GAC	TTG	ATC	TTT	GGC	CTA	AAT	GCG	TTA	TTA	638
Ala	Asn	Cys	Ser	Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu	Leu	
				180				185					190			
AGA	ACA	GCA	GAT	TTG	CAG	TGG	AAC	AGT	TCT	AAT	GCT	CAG	TTG	CTC	CTG	686
Arg	Thr	Ala	Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu	
				195			200					205				
GAC	TAC	TGC	TCT	TCC	AAG	GGG	TAT	AAC	ATT	TCT	TGG	GAA	CTA	GGC	AAT	734
Asp	Tyr	Cys	Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn	
				210		215					220					
GAA	CCT	AAC	AGT	TTC	CTT	AAG	AAG	GCT	GAT	ATT	TTC	ATC	AAT	GGG	TCG	782
Glu	Pro	Asn	Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	Ser	
225					230				235					240		
CAG	TTA	GGA	GAA	GAT	TAT	ATT	CAA	TTG	CAT	AAA	CTT	CTA	AGA	AAG	TCC	830
Gln	Leu	Gly	Glu	Asp	Tyr	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	Ser	
				245					250					255		
ACC	TTC	AAA	AAT	GCA	AAA	CTC	TAT	GGT	CCT	GAT	GTT	GGT	CAG	CCT	CGA	878
Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	Arg	
				260				265					270			
AGA	AAG	ACG	GCT	AAG	ATG	CTG	AAG	AGC	TTC	CTG	AAG	GCT	GGT	GGA	GAA	926
Arg	Lys	Thr	Ala	Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	Glu	
				275			280					285				
GTG	ATT	GAT	TCA	GTT	ACA	TGG	CAT	CAC	TAC	TAT	TTG	AAT	GGA	CGG	ACT	974
Val	Ile	Asp	Ser	Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	Thr	
				290		295					300					
GCT	ACC	AGG	GAA	GAT	TTT	CTA	AAC	CCT	GAT	GTA	TTG	GAC	ATT	TTT	ATT	1022
Ala	Thr	Arg	Glu	Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	Ile	
305					310					315					320	
TCA	TCT	GTG	CAA	AAA	GTT	TTC	CAG	GTG	GTT	GAG	AGC	ACC	AGG	CCT	GGC	1070
Ser	Ser	Val	Gln	Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	Gly	
				325				330						335		
AAG	AAG	GTC	TGG	TTA	GGA	GAA	ACA	AGC	TCT	GCA	TAT	GGA	GGC	GGA	GCG	1118
Lys	Lys	Val	Trp	Leu	Gly	Glu	Thr	Ser	Ser	Ala	Tyr	Gly	Gly	Gly	Ala	
				340				345					350			
CCC	TTG	CTA	TCC	GAC	ACC	TTT	GCA	GCT	GGC	TTT	ATG	TGG	CTG	GAT	AAA	1166
Pro	Leu	Leu	Ser	Asp	Thr	Phe	Ala	Ala	Gly	Phe	Met	Trp	Leu	Asp	Lys	
				355			360					365				
TTG	GGC	CTG	TCA	GCC	CGA	ATG	GGA	ATA	GAA	GTG	GTG	ATG	AGG	CAA	GTA	1214
Leu	Gly	Leu	Ser	Ala	Arg	Met	Gly	Ile	Glu	Val	Val	Met	Arg	Gln	Val	
				370		375					380					
TTC	TTT	GGA	GCA	GGA	AAC	TAC	CAT	TTA	GTG	GAT	GAA	AAC	TTC	GAT	CCT	1262
Phe	Phe	Gly	Ala	Gly	Asn	Tyr	His	Leu	Val	Asp	Glu	Asn	Phe	Asp	Pro	
385					390					395				400		
TTA	CCT	GAT	TAT	TGG	CTA	TCT	CTT	CTG	TTC	AAG	AAA	TTG	GTG	GGC	ACC	1310
Leu	Pro	Asp	Tyr	Trp	Leu	Ser	Leu	Leu	Phe	Lys	Lys	Leu	Val	Gly	Thr	
				405				410						415		
AAG	GTG	TTA	ATG	GCA	AGC	GTG	CAA	GGT	TCA	AAG	AGA	AGG	AAG	CTT	CGA	1358
Lys	Val	Leu	Met	Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	Arg	
				420				425					430			
GTA	TAC	CTT	CAT	TGC	ACA	AAC	ACT	GAC	AAT	CCA	AGG	TAT	AAA	GAA	GGA	1406
Val	Tyr	Leu	His	Cys	Thr	Asn	Thr	Asp	Asn	Pro	Arg	Tyr	Lys	Glu	Gly	
				435			440					445				
GAT	TTA	ACT	CTG	TAT	GCC	ATA	AAC	CTC	CAT	AAC	GTC	ACC	AAG	TAC	TTG	1454
Asp	Leu	Thr	Leu	Tyr	Ala	Ile	Asn	Leu	His	Asn	Val	Thr	Lys	Tyr	Leu	
				450		455					460					
CGG	TTA	CCC	TAT	CCT	TTT	TCT	AAC	AAG	CAA	GTG	GAT	AAA	TAC	CTT	CTA	1502

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu  
 465 470 475 480

AGA CCT TTG GGA CCT CAT GGA TTA CTT TCC AAA TCT GTC CAA CTC AAT 1550  
 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn  
 485 490 495

GGT CTA ACT CTA AAG ATG GTG GAT GAT CAA ACC TTG CCA CCT TTA ATG 1598  
 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met  
 500 505 510

GAA AAA CCT CTC CGG CCA GGA AGT TCA CTG GGC TTG CCA GCT TTC TCA 1646  
 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser  
 515 520 525

TAT AGT TTT TTT GTG ATA AGA AAT GCC AAA GTT GCT GCT TGC ATC TGA 1694  
 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile  
 530 535 540 543

AAA TAA AAT ATA CTA GTC CTG ACA CTG 1721

- (2) INFORMATION FOR SEQ ID NO:4:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
 CGCATATGCA GGACGTCGTG GACCTG 26
- (2) INFORMATION FOR SEQ ID NO:5:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
 TATGATCCTC TAGTACTTCT CGAC 24
- (2) INFORMATION FOR SEQ ID NO:6:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
 TTCGATCCCA AGAAGGAATC AAC 23
- (2) INFORMATION FOR SEQ ID NO:7:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
 GTAGTGATGC CATGTAATG AATC 24

604460 23544550